SEQUENCE LISTING

<110> Curiel, David T.
Krasnykh, Victor N.

<120> Modified Adenovirus Containing A Fiber Replacement Protein

<130> D6070CIP

<141> 2000-07-10

<150> US 09/250,580
US 60/074,844

<151> 1999-02-16
1998-02-17

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<212> DNA
<213> artificial sequence
<220>
<221> primer_bind
<223> Forward primer FF.F used to amplify segment of the T4 fibritin gene encoding amino acids Ser-229 through the carboxy terminal Ala-487.

<400> 1
gggaacttga cctcacagaa cgtttatagt cgtttaaatg 40

<210> 2
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<223> Reverse primer FF.R used to amplify segment of the T4 fibritin gene encoding amino acids Ser-229 through the carboxy terminal Ala-487.

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aggccatggc caatttttgc cggcgataaa aaggtag 37

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<223> synthetic oligo, F5.Δ3Swa.T, for the introduction of SwaI restriction site
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ttggccccat ttaaatgaat cgtttgtgtt atgtttcaac gtgtttattt ttc 53

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aattgaaaaa taaacacgtt gaaacataac acaaacgatt catttaaatg 50
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ggcaggtgga ggcggttcag gcggaggtgg ctctggcggt ggcggatccg 50
gggattt 57

<210> 6

<211> 57
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<221> primer_bind
<223> primer to PCR amplify FF/6H in pXK.FF/6H

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ccctcatgaa gcgcgcaaga ccgtctg 27

<210> 10
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cccaagctta gtgatggtga tggtgat 27

<210> 11
<211> 8
<212> PRT
<213> Adenovirus type 5
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<221> DOMAIN
<223> the beginning of the third pseudorepeat of the fiber shaft domain
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Gly Asn Thr Leu Ser Gln Asn Val
5 8

<210> 12
<211> 26
<212> PRT
<213> Phage T4
<220>
<221> DOMAIN
<223> the sixth coiled coil segment of the α-helical central domain of the fibritin
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Val Tyr Ser Arg Leu Asn Glu Ile Asp Thr Lys Gln Thr Thr Val
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Glu Ser Asp Ile Ser Ala Ile Lys Thr Ser Ile
20 25

<210> 13
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<212> PRT
<213> artificial sequence
<220>
<221> CHAIN
<223> the fiber-fibritin-6H chimera
<400> 13

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr
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Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr
20 25 30
Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
35 40 45
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly
50 55 60
Met Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly
65 70 75
Asn Leu Thr Ser Gln Asn Val Tyr Ser Arg Leu Asn Glu Ile Asp
80 85 90
Thr Lys Gln Thr Thr Val Glu Ser Asp Ile Ser Ala Ile Lys Thr
95 100 105
Ser Ile Gly Tyr Pro Gly Asn Asn Ser Ile Ile Thr Ser Val Asn
110 115 120
Thr Asn Thr Asp Asn Ile Ala Ser Ile Asn Leu Glu Leu Asn Gln
125 130 135
Ser Gly Gly Ile Lys Gln Arg Leu Thr Val Ile Glu Thr Ser Ile
140 145 150
Gly Ser Asp Asp Ile Pro Ser Ser Ile Lys Gly Gln Ile Lys Asp
155 160 165
Asn Thr Thr Ser Ile Glu Ser Leu Asn Gly Ile Val Gly Glu Asn
170 175 180
Thr Ser Ser Gly Leu Arg Ala Asn Val Ser Trp Leu Asn Gln Ile

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Val Gly Thr Asp Ser Ser Gly Gly Gln Pro Ser Pro Pro Gly Ser
                200                 205                 210
Leu Leu Asn Arg Val Ser Thr Ile Glu Thr Ser Val Ser Gly Leu
                215                 220                 225
Asn Asn Asp Val Gln Asn Leu Gln Val Glu Ile Gly Asn Asn Ser
                230                 235                 240
Thr Gly Ile Lys Gly Gln Val Val Ala Leu Asn Thr Leu Val Asn
                245                 250                 255
Gly Thr Asn Pro Asn Gly Ser Thr Val Glu Glu Arg Gly Leu Thr
                260                 265                 270
Asn Ser Ile Lys Ala Asn Glu Thr Asn Ile Ala Ser Val Thr Gln
                275                 280                 285
Glu Val Asn Thr Ala Lys Gly Asn Ile Ser Ser Leu Gln Gly Asp
                290                 295                 300
Val Gln Ala Leu Gln Glu Ala Gly Tyr Ile Pro Glu Ala Pro Arg
                305                 310                 315
Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
                320                 325                 330
Ser Thr Phe Leu Ser Pro Ala Gly Gly Gly Gly Ser Gly Gly Gly
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Gly Ser Gly Gly Gly Gly Ser Arg Gly Ser His His His His His
                350                 355                 360
His
361
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<212> PRT
<213> Unknown
<220>
<221> DOMAIN
<223> a peptide ligand containing the RGD motif
<400> 14

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SEQ 6